WHAT IS CLAIMED IS:

1. A method of determining whether a member of a pool of test transcription factor polynucleotides encodes a pathway transcription factor, the method comprising introducing into a cell a nucleic acid comprising a pathway gene promoter operably linked to a reporter gene and a pool of nucleic acid members comprising test transcription factor polynucleotides and detecting expression from said pathway gene promoter in the cell, thereby determining whether a member of the test transcription factor polynucleotide pool encodes a pathway transcription factor.

2. The method of claim 1, wherein a member of the test transcription factor nucleic acid pool is selected on the basis of structural similarity to a known transcription factor for a pathway gene.

3. The method of claim 1, wherein a member of the test transcription factor nucleic acid pool is selected without regard to structural similarity to a known transcription factor for a pathway gene.

4. The method of claim 1, further comprising detecting the expression of at least one other pathway gene in the cell.

5. The method of claim 1, wherein said pathway gene is a biosynthetic pathway gene.

6. The method of claim 5, wherein said biosynthetic pathway gene is a primary metabolite pathway gene.

7. The method of claim 5, wherein said biosynthetic pathway gene is a secondary metabolite pathway gene.

8. The method of claim 7, wherein said secondary metabolite pathway gene is a terpenoid pathway gene.

9. The method of claim 7, wherein said secondary metabolite pathway gene is an alkaloid pathway gene.

10. The method of claim 1, wherein said test transcription factor polynucleotide is from a plant.

11. The method of claim 1, wherein said test transcription factor polynucleotide is expressed transiently in the cell.

12. The method of claim 1, wherein said cell is from a plant.

13. The method of claim 1, wherein said promoter is operably linked to a reporter gene is transiently transfected into a cell.

14. The method of claim 1, wherein said reporter gene is GUS.

15. The method of claim 1, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces high-value metabolites.

16. The method of claim 8, wherein said terpenoid pathway gene is from a species selected from the group consisting of *Mentha* and *Taxus*.

17. The method of claim 8, wherein said terpenoid pathway gene is selected from the group consisting of limonene synthase and taxadiene synthase.

18 The method of claim 1, further comprising deconvoluting the pool of nucleic acid members to identify the minimum number of test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter.

19. A method of determining whether a member of a pool of test transcription factor polynucleotides encodes a transcription factor for a biosynthetic pathway gene, comprising introducing into a cell a pool of nucleic acid members comprising test transcription factor polynucleotides and detecting accumulation of metabolites in the cell.

20. The method of claim 19, wherein said biosynthetic pathway gene is a primary metabolite pathway gene.

21. The method of claim 19, wherein said biosynthetic pathway gene is a secondary metabolite pathway gene.

22. The method of claim 21, wherein said secondary metabolite pathway gene is a terpenoid pathway gene.

23. The method of claim 21, wherein said secondary metabolite pathway gene is an alkaloid gene.

24. The method of claim 19, wherein said cell is from a species selected from the group consisting of *Mentha* and *Taxus*.

25. A method of determining whether a member of a pool of test transcription factor polynucleotides encodes a transcription factor for a terpenoid pathway gene, comprising introducing into a cell a pool of nucleic acid members comprising test transcription factor polynucleotides and detecting accumulation of terpenoids in the cell.

26. A method of determining whether a member of a pool of test transcription factor polynucleotides encodes a biosynthetic pathway transcription factor, comprising introducing into a cell nucleic acids comprising the test transcription factor polynucleotides and detecting expression of a biosynthetic pathway gene in the cell by quantitation of the biosynthetic pathway gene RNA level.

27. A transgenic plant or plant cell comprising a nucleic acid encoding a pathway transcription factor identified by the method of claim 1.

28. The transgenic plant or plant cell of claim 27 comprising a comprising a pathway transcription factor selected from the group consisting of :

(a) a polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOs. 1, 3, 5 and 7; and

(b) a polynucleotide encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs. 2, 4, 6, and 8.

29. A method of isolating a metabolite, the method comprising:

a) providing a plant cell or plant of claim 28; and

b) isolating the metabolite from said plant cell or plant.

30. The method of claim 29, wherein said metabolite is a primary or secondary metabolite.

31. The method of claim 30, wherein said secondary metabolite is a terpenoid or an alkaloid.

32. The method of claim 29, wherein said plant cell or whole plant is selected from a species selected from the group of *Mentha* and *Taxus*.

33. A method of determining whether two or more members of a pool of test transcription factor polynucleotides are required for expression from a pathway gene promoter, the method comprising introducing into a cell a nucleic acid comprising a pathway gene promoter operably linked to a reporter gene and a pool of nucleic acid members comprising test transcription factor polynucleotides and detecting expression from said biosynthetic pathway gene promoter in the cell, thereby determining whether two or more members of the test transcription factor polynucleotide pool are required for expression from said pathway promoter.

34. The method of claim 33, further comprising deconvoluting the pool of nucleic acid members to identify the minimum number of test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter.

35. The method of claim 33, wherein a member of the test transcription factor nucleic acid pool is selected on the basis of structural similarity to a known transcription factor for a pathway gene.

36. The method of claim 33, wherein a member of the test transcription factor nucleic acid pool is selected without regard to structural similarity to a known transcription factor for a pathway gene.

37. The method of claim 33, further comprising detecting the expression of at least one other pathway gene in the cell.

38. The method of claim 33, wherein said pathway gene is a biosynthetic pathway gene.

39. The method of claim 38, wherein said biosynthetic pathway gene is a primary metabolite pathway gene.

40. The method of claim 38, wherein said biosynthetic pathway gene is a secondary metabolite pathway gene.

41. The method of claim 40, wherein said secondary metabolite pathway gene is a terpenoid pathway gene.

42. The method of claim 40, wherein said secondary metabolite pathway gene is an alkaloid pathway gene.

43. The method of claim 33, wherein said test transcription factor polynucleotide is from a plant.

44. The method of claim 33, wherein said test transcription factor polynucleotide is expressed transiently in the cell.

45. The method of claim 33, wherein said cell is from a plant.

46. The method of claim 33, wherein said promoter is operably linked to a reporter gene is transiently transfected into a cell.

47. The method of claim 46, wherein said reporter gene is GUS.

48. The method of claim 33, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces high-value metabolites.

49. The method of claim 41, wherein said terpenoid pathway gene is from a species selected from the group consisting of *Mentha* and *Taxus*.

50. The method of claim 41, wherein said terpenoid pathway gene is selected from the group consisting of limonene synthase and taxadiene synthase.